Amendments to the Specification:

Please amend the paragraph beginning at page 6, line 6, as follows:

Fig. 1 shows a sequence of an initial RNA pool in the in vitro selection of the present invention (SEQ ID NO:61) and sequences of PCR primers 1 and 2 (SEQ ID NOs:58 and 58, respectively).

Please amend the paragraph beginning at page 6, line 9, as follows:

Fig. 2 shows 24 sequences of RNAs obtained from the RNA pool in the 21st round. In the drawing, a random sequence moiety of approximately 60 bases is shown. The overall sequence include the sequences of the 5'- and 3'- termini defined in Fig. 1. Sequences which are the same as that of clone 1 are termed "group 1" (SEQ ID NOs:29-36). The other sequences are termed "group 2" (SEQ ID NOs:37-52). Incidentally, in note (a), the number of clones of ligands isolated respectively is shown in parentheses. In note (b), clone 21.08 (SEQ ID NO:36) indicates that each sequence defined has two mutations. In note (c) , percentage of the binding of the RNA ligand to GST-RBD is based on a value measured by the nitrocellulose filter binding assay. Clone 21.01: SEQ ID NO:29. Clone 21.02: SEQ ID NO:30. Clone 21.03: SEQ ID NO:31. Clone 21.04: SEQ ID NO:32. Clone 21.05: SEQ ID NO:33. Clone 21.06: SEQ ID NO:34. Clone 21.07: SEQ ID NO:35. Clone 21.08: SEQ ID NO:36. Clone 21.09: SEQ ID NO:37. Clone 21.10: SEQ ID NO:38. Clone 21.11: SEQ ID NO:39. Clone 21.12: SEQ ID NO:40. Clone 21.13: SEQ ID NO:41. Clone 21.14: SEQ ID NO:42. Clone 21.15: SEQ ID NO:43. Clone 21.16: SEQ ID NO:44. Clone 21.17: SEQ ID NO:45. Clone 21.18: SEQ ID NO:46. Clone 21.19: SEQ ID NO:47. Clone 21.20: SEQ ID NO:48. Clone 21.21: SEQ ID NO:49. Clone 21.22: SEQ ID NO:50. Clone 21.23: SEQ ID NO:51. Clone 21.24: SEQ ID NO:52.

Please amend the paragraph beginning at page 21, line 7, as follows:

A pool of DNAs containing random 60 bases was prepared. These DNAs have sequences 5'-GCCGGAATTCTAATACGACTCACTATAGGGAGATCAGAATAAACGCTCAA-3' (SEQ ID NO:57) and 5'-TTCGACATGAGGCCCCTGCAGGGCG-3' (SEQ ID NO:62) at both termini for in vitro transcription and amplification by PCR.

Please amend the paragraph beginning at page 23, line 4 from the bottom of the page, as follows:

A single-stranded DNA (200 pmols, 1.2×10^{14} molecules) containing random 45 bases and having a sequence 5'-ggtaa tacga ctcac tatag ggagt ggagg aattc atcga ggcat-3' (SEQ ID NO:59) at the 5' terminus and a sequence 5'-catat gcctt agcga cagca agctt ctgc-3' (SEQ ID NO:60) at the 3'-terminus was subjected to PCR using 2 primers, 5'-ggtaa tacga ctcac tatag ggagt ggagg aattc atcg-3'(SEQ ID NO:63) and 5'-gcaga agctt gctgt cgcta aggc-3'(SEQ ID NO:64), and then transcribed with a T7 RNA polymerase to form a first RNA pool.

Please amend the paragraph beginning at page 25, line 7 from the bottom of the page, as follows:

DNAs which had a complementary sequence of an RNA of sequence no. 25 and of which the 3-terminus side was shortened were obtained by PCR using a primer 5'-ggtaa tacga ctcac tatag ~~ggaggt~~ ggagt ggagg aattc atcg-3' (SEQ ID NO:63) and a primer 5'-gctgt cgcta aggca tatgc taaaa c-3' (SEQ ID NO:65) or 5'-aggca tatgc taaaa ccaat ttata ac-3' (SEQ ID NO:66). From these DNAs, RNAs of sequence Nos. 27 and 28 of Sequence Listing were obtained.